AMENDMENTS TO THE CLAIMS;

This listing of claims will replace all prior versions and listing of the claims in the application:

LISTING OF THE CLAIMS:

Claim 1. (Currently amended) A method for preparing a population of variant polynucleotides having a nucleotide sequence not identical to either of at least two parent polynucleotides comprising;

preparing at least one heteroduplex between said at least two parent polynucleotides having at least 75% sequence identity wherein said heteroduplex has at least two mismatch sites separated by at least one complementary nucleotide base pair,

cleaving at least one polynucleotide strand in said heteroduplex within six nucleotides 3' of a mismatch site with an effective amount of an endonuclease having mismatch-directed strand cleavage activity to form a cleavage site ~~wherein said mismatch-directed strand cleavage activity is a mismatch endonuclease~~,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site,

wherein ~~at least one~~ polynucleotide strands ~~is~~ are formed that ~~has~~ have a nucleotide sequence not identical to either of said at least two parent polynucleotides or the complementary sequences of said at least two parent polynucleotides forming a population of polynucleotides containing sequence variants, and at least 44% of the population has undergone reassortment of sequence information and the sequence variants have an average of 1 or more crossovers per 95 basepairs of heteroduplex polynucleotide sequence.

Claim 2. (Original) The method of claim 1 wherein the polynucleotides forming a heteroduplex are circular.

Claim 3. (Canceled)

Claim 4. (Previously presented) The method of claim 1 wherein said at least one heteroduplex contains a gene.

Claim 5. (Previously presented) The method of claim 4 wherein said at least one heteroduplex is a genome.

Claim 6. (Canceled)

Claim 7. (Currently amended) A method for preparing a population of variant polynucleotide strands having a nucleotide sequence not identical to any of at least three parent polynucleotides comprising;

preparing at least two different heteroduplexes among said at least three parent polynucleotides wherein each of said at least two different heteroduplexes has at least two mismatch sites separated by at least one complementary nucleotide base pair,

cleaving ~~at least one~~ polynucleotide strands in said heteroduplexes within six nucleotides 3' of ~~a~~ mismatch sites with an effective amount of an endonuclease having mismatch-directed strand cleavage activity to form ~~a~~ cleavage sites~~ wherein said mismatch-directed strand cleavage activity is a mismatch endonuclease~~,

replacing ~~at least one~~ nucleotides on ~~at least one~~ polynucleotide strands at or near the cleavage sites,

wherein ~~at least one~~ variant polynucleotide strands are ~~is~~ formed that ~~has~~ have a nucleotide sequence not identical to any of said at least three parent polynucleotides or the complementary sequences of said at least three parent polynucleotides, and a population of said variant polynucleotide strands is formed wherein at least 20% of the population has undergone reassortment of sequence information and the variant polynucleotide strands have an average of 1 or more crossovers per 250 basepairs relative to the heteroduplex polynucleotide sequence.

Claim 8. (Canceled) ~~The method of claim 1 wherein a plurality of variant polynucleotides is formed.~~

Claim 9. (Currently amended) A method for obtaining polynucleotide sequence variants encoding a desired functional property comprising;

preparing at least one heteroduplex from at least two parent polynucleotides;

cleaving at least one polynucleotide strand in said heteroduplexes within six nucleotides 3' of a mismatch site with an effective amount of an endonuclease having mismatch-directed strand cleavage activity to form a cleavage site ~~wherein said mismatch-directed strand cleavage activity is a mismatch endonuclease~~,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site, wherein a plurality of variant polynucleotide strands is formed which have nucleotide sequences not identical to either of said at least two parent polynucleotides or the complementary sequences of said at least two parent polynucleotides to form a population of variants wherein at least 20% of the population has undergone reassortment of sequence information and the sequence variants have an average of 1 or more crossovers per 250 basepairs of heteroduplex polynucleotide sequence, and

screening or selecting said population of variants for the desired functional property.

Claim 10. (Previously presented) The method of claim 9 further comprising;

forming a second heteroduplex containing at least one variant polynucleotide strand,

cleaving at least one polynucleotide strand in said second heteroduplex within six nucleotides 3' of a mismatch site to form a cleavage site,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site, wherein a plurality of variant polynucleotide strands is formed which have nucleotide sequences not identical to either parent polynucleotide or the complementary sequences of either parent polynucleotide present in said second heteroduplex to form a population of variants, and

screening or selecting said population of variants for the desired functional property.

Claim 11. (Original) The method of claim 9 further comprising converting said variant polynucleotide to RNA before said screening or selecting.

Claim 12. (Original) The method of claim 9 further comprising translating said variant polynucleotide or an RNA transcribed therefrom to produce a polypeptide and wherein said screening or selecting is performed on said polypeptide.

Claims 13-43 (Canceled)